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PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/890,677

DATE: 01/19/2002
TIME: 11:50:27

Input Set : A:\7410.ST25.txt
Output Set: N:\CRF3\01182002\I890677.raw

ENTERED

3 <110> APPLICANT: The Procter & Gamble Company
4 Smerznak, Mark A.
5 Broeckx, Walter A. M.
6 Johnston, James P.
7 Fredj, Abdennaceur
9 <120> TITLE OF INVENTION: Low Density Enzyme Granulates and Compositions Employing
Same
11 <130> FILE REFERENCE: 7410
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/890,677
C--> 13 <141> CURRENT FILING DATE: 2001-12-19
13 <160> NUMBER OF SEQ ID NOS: 7
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1497
19 <212> TYPE: DNA
20 <213> ORGANISM: bacillus amyloliquefaciens
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (96)..(1241)
25 <223> OTHER INFORMATION:
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31 ttattctgca aatgaaaaaa aggagaggat aaaga gtg aga ggc aaa aaa gta 113
32 Val Arg Gly Lys Lys Val
33 1 5
35 tgg atc agt ttg ctg ttt gct tta gcg tta atc ttt acg atg gcg ttc 161
36 Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu Ile Phe Thr Met Ala Phe
37 10 15 20
39 ggc agc aca tcc tct gcc cag gcg gca ggg aaa tca aac ggg gaa aag 209
40 Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys
41 25 30 35
43 aaa tat att gtc ggg ttt aaa cag aca atg agc acg atg agc gcc gct 257
44 Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met Ser Ala Ala
45 40 45 50
47 aag aag aaa gat gtc att tct gaa aaa ggc ggg aaa gtg caa aag caa 305
48 Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly Lys Val Gln Lys Gln
49 55 60 65 70
51 ttc aaa tat gta gac gca gct tca gtc aca tta aac gaa aaa gct gta 353
52 Phe Lys Tyr Val Asp Ala Ala Ser Val Thr Leu Asn Glu Lys Ala Val
53 75 80 85
55 aaa gaa ttg aaa aaa gac ccg agc gtc gct tac gtt gaa gaa gat cac 401
56 Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His
57 90 95 100
59 gta gca cat gcg tac gcg cag tcc gtg cct tac ggc gta tca caa att 449

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60 Val Ala His Ala Tyr Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile
61      105      110      115
63 aaa gcc cct gct ctg cac tct caa ggc tac act gga tca aat gtt aaa      497
64 Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys
65      120      125      130
67 gta gcg gtt atc gac agc ggt atc gat tct tct cat cct gat tta aag      545
68 Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys
69 135      140      145      150
71 gta gca agc gga gcc agc atg gtt cct tct gaa aca aat cct ttc caa      593
72 Val Ala Ser Gly Ala Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln
73      155      160      165
75 gac aac aac tct cac gga act cac gtt gcc ggc aca gtt gcg gct ctt      641
76 Asp Asn Asn Ser His Gly Thr His Val Ala Gly Thr Val Ala Ala Leu
77      170      175      180
79 aat aac tca atc ggt gta tta ggc gtt gcg cca agc gca tca ctt tac      689
80 Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr
81      185      190      195
83 gct gta aaa gtt ctc ggt gct gac ggt tcc ggc caa tac agc tgg atc      737
84 Ala Val Lys Val Leu Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile
85      200      205      210
87 att aac gga atc gag tgg gcg atc gca aac aat atg gac gtt att aac      785
88 Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn
89 215      220      225      230
91 atg agc ctc ggc gga cct tct ggt tct gct gct tta aaa gcg gca gtt      833
92 Met Ser Leu Gly Gly Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val
93      235      240      245
95 gat aaa gcc gtt gca tcc ggc gtc gta gtc gtt gcg gca gcc ggt aac      881
96 Asp Lys Ala Val Ala Ser Gly Val Val Val Val Ala Ala Ala Gly Asn
97      250      255      260
99 gaa ggc act tcc ggc agc tca agc aca gtg ggc tac cct ggt aaa tac      929
100 Glu Gly Thr Ser Gly Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr
101      265      270      275
103 cct tct gtc att gca gta ggc gct gtt gac agc agc aac caa aga gca      977
104 Pro Ser Val Ile Ala Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala
105      280      285      290
107 tct ttc tca agc gta gga cct gag ctt gat gtc atg gca cct ggc gta      1025
108 Ser Phe Ser Ser Val Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val
109 295      300      305      310
111 tct atc caa agc acg ctt cct gga aac aaa tac ggg gcg tac aac ggt      1073
112 Ser Ile Gln Ser Thr Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly
113      315      320      325
115 acg tca atg gca tct ccg cac gtt gcc gga gcg gct gct ttg att ctt      1121
116 Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu
117      330      335      340
119 tct aag cac ccg aac tgg aca aac act caa gtc cgc agc agt tta gaa      1169
120 Ser Lys His Pro Asn Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu
121      345      350      355
123 aac acc act aca aaa ctt ggt gat tct ttg tac tat gga aaa ggg ctg      1217
124 Asn Thr Thr Thr Lys Leu Gly Asp Ser Leu Tyr Tyr Gly Lys Gly Leu

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125      360      365      370
127 atc aac gta caa gcg gca gct cag taaaacataa aaaaccggcc ttggccccgc      1271
128 Ile Asn Val Gln Ala Ala Ala Gln
129 375      380
131 cggtttttta ttatttttct tcctccgcat gttcaatccg ctccataatc gacggatggc      1331
133 tcctcttgaa aattttaacg agaaacggcg ggttgaccgc gctcagtcgc gtaacggcca      1391
135 actcctgaaa cgtctcaatc gcgccttccc ggtttccggt cagctcaatg ccataacggt      1451
137 cggcggcggt ttcttgatac cgggagacgg cattcgtaat cggatc      1497
140 <210> SEQ ID NO: 2
141 <211> LENGTH: 382
142 <212> TYPE: PRT
143 <213> ORGANISM: bacillus amyloliquefaciens
145 <400> SEQUENCE: 2
147 Val Arg Gly Lys Lys Val Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu
148 1      5      10      15
151 Ile Phe Thr Met Ala Phe Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly
152      20      25      30
155 Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met
156      35      40      45
159 Ser Thr Met Ser Ala Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly
160      50      55      60
163 Gly Lys Val Gln Lys Gln Phe Lys Tyr Val Asp Ala Ala Ser Val Thr
164 65      70      75      80
167 Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala
168      85      90      95
171 Tyr Val Glu Glu Asp His Val Ala His Ala Tyr Ala Gln Ser Val Pro
172      100     105     110
175 Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr
176      115     120     125
179 Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser
180      130     135     140
183 Ser His Pro Asp Leu Lys Val Ala Ser Gly Ala Ser Met Val Pro Ser
184 145     150     155     160
187 Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His Gly Thr His Val Ala
188      165     170     175
191 Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala
192      180     185     190
195 Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu Gly Ala Asp Gly Ser
196      195     200     205
199 Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn
200      210     215     220
203 Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Ala
204 225     230     235     240
207 Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala Ser Gly Val Val Val
208      245     250     255
211 Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly Ser Ser Ser Thr Val
212      260     265     270
215 Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala Val Gly Ala Val Asp
216      275     280     285

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219 Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val Gly Pro Glu Leu Asp
220      290      295      300
223 Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr Leu Pro Gly Asn Lys
224 305      310      315      320
227 Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser Pro His Val Ala Gly
228      325      330      335
231 Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn Trp Thr Asn Thr Gln
232      340      345      350
235 Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys Leu Gly Asp Ser Leu
236      355      360      365
239 Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala Ala Gln
240      370      375      380
243 <210> SEQ ID NO: 3
244 <211> LENGTH: 1497
245 <212> TYPE: PRT
246 <213> ORGANISM: bacillus amyloliquefaciens
248 <400> SEQUENCE: 3
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251 1      5      10      15
254 Ala Thr Thr Cys Cys Ala Thr Ala Cys Thr Ala Thr Ala Cys Ala Ala
255      20      25      30
258 Thr Thr Ala Ala Thr Ala Cys Ala Cys Ala Gly Ala Ala Thr Ala Ala
259      35      40      45
262 Thr Cys Thr Gly Thr Cys Thr Ala Thr Thr Gly Gly Thr Thr Ala Thr
263      50      55      60
266 Thr Cys Thr Gly Cys Ala Ala Ala Thr Gly Ala Ala Ala Ala Ala Ala
267 65      70      75      80
270 Ala Gly Gly Ala Gly Ala Gly Gly Ala Thr Ala Ala Ala Gly Ala Gly
271      85      90      95
274 Thr Gly Ala Gly Ala Gly Gly Cys Ala Ala Ala Ala Ala Ala Gly Thr
275      100      105      110
278 Ala Thr Gly Gly Ala Thr Cys Ala Gly Thr Thr Thr Gly Cys Thr Gly
279      115      120      125
282 Thr Thr Thr Gly Cys Thr Thr Ala Gly Cys Gly Thr Thr Ala Ala
283      130      135      140
286 Thr Cys Thr Thr Thr Ala Cys Gly Ala Thr Gly Gly Cys Gly Thr Thr
287 145      150      155      160
290 Cys Gly Gly Cys Ala Gly Cys Ala Cys Ala Thr Cys Cys Thr Cys Thr
291      165      170      175
294 Gly Cys Cys Cys Ala Gly Gly Cys Gly Gly Cys Ala Gly Gly Gly Ala
295      180      185      190
298 Ala Ala Thr Cys Ala Ala Ala Cys Gly Gly Gly Gly Ala Ala Ala Ala
299      195      200      205
302 Gly Ala Ala Ala Thr Ala Thr Ala Thr Thr Gly Thr Cys Gly Gly Gly
303      210      215      220
306 Thr Thr Thr Ala Ala Ala Cys Ala Gly Ala Cys Ala Ala Thr Gly Ala
307 225      230      235      240
310 Gly Cys Ala Cys Gly Ala Thr Gly Ala Gly Cys Gly Cys Cys Gly Cys
311      245      250      255

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314 Thr Ala Ala Gly Ala Ala Gly Ala Ala Ala Gly Ala Thr Gly Thr Cys
315          260          265          270
318 Ala Thr Thr Thr Cys Thr Gly Ala Ala Ala Ala Ala Gly Gly Cys Gly
319          275          280          285
322 Gly Gly Ala Ala Ala Gly Thr Gly Cys Ala Ala Ala Ala Gly Cys Ala
323          290          295          300
326 Ala Thr Thr Cys Ala Ala Ala Thr Ala Thr Gly Thr Ala Gly Ala Cys
327 305          310          315          320
330 Gly Cys Ala Gly Cys Thr Thr Cys Ala Gly Thr Cys Ala Cys Ala Thr
331          325          330          335
334 Thr Ala Ala Ala Cys Gly Ala Ala Ala Ala Ala Gly Cys Thr Gly Thr
335          340          345          350
338 Ala Ala Ala Ala Gly Ala Ala Thr Thr Gly Ala Ala Ala Ala Ala
339          355          360          365
342 Gly Ala Cys Cys Cys Gly Ala Gly Cys Gly Thr Cys Gly Cys Thr Thr
343          370          375          380
346 Ala Cys Gly Thr Thr Gly Ala Ala Gly Ala Ala Gly Ala Thr Cys Ala
347 385          390          395          400
350 Cys Gly Thr Ala Gly Cys Ala Cys Ala Thr Gly Cys Gly Thr Ala Cys
351          405          410          415
354 Gly Cys Gly Cys Ala Gly Thr Cys Cys Gly Thr Gly Cys Cys Thr Thr
355          420          425          430
358 Ala Cys Gly Gly Cys Gly Thr Ala Thr Cys Ala Cys Ala Ala Ala Thr
359          435          440          445
362 Thr Ala Ala Ala Gly Cys Cys Cys Cys Thr Gly Cys Thr Cys Thr Gly
363          450          455          460
366 Cys Ala Cys Thr Cys Thr Cys Ala Ala Gly Gly Cys Thr Ala Cys Ala
367 465          470          475          480
370 Cys Thr Gly Gly Ala Thr Cys Ala Ala Ala Thr Gly Thr Thr Ala Ala
371          485          490          495
374 Ala Gly Thr Ala Gly Cys Gly Gly Thr Thr Ala Thr Cys Gly Ala Cys
375          500          505          510
378 Ala Gly Cys Gly Gly Thr Ala Thr Cys Gly Ala Thr Thr Cys Thr Thr
379          515          520          525
382 Cys Thr Cys Ala Thr Cys Cys Thr Gly Ala Thr Thr Thr Ala Ala Ala
383          530          535          540
386 Gly Gly Thr Ala Gly Cys Ala Ala Gly Cys Gly Gly Ala Gly Cys Cys
387 545          550          555          560
390 Ala Gly Cys Ala Thr Gly Gly Thr Thr Cys Cys Thr Thr Cys Thr Gly
391          565          570          575
394 Ala Ala Ala Cys Ala Ala Ala Thr Cys Cys Thr Thr Thr Cys Cys Ala
395          580          585          590
398 Ala Gly Ala Cys Ala Ala Cys Ala Ala Cys Thr Cys Thr Cys Ala Cys
399          595          600          605
402 Gly Gly Ala Ala Cys Thr Cys Ala Cys Gly Thr Thr Gly Cys Cys Gly
403          610          615          620
406 Gly Cys Ala Cys Ala Gly Thr Thr Gly Cys Gly Gly Cys Thr Cys Thr
407 625          630          635          640
410 Thr Ala Ala Thr Ala Ala Cys Thr Cys Ala Ala Thr Cys Gly Gly Thr

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/890,677

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Input Set : A:\7410.ST25.txt

Output Set: N:\CRF3\01182002\I890677.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date